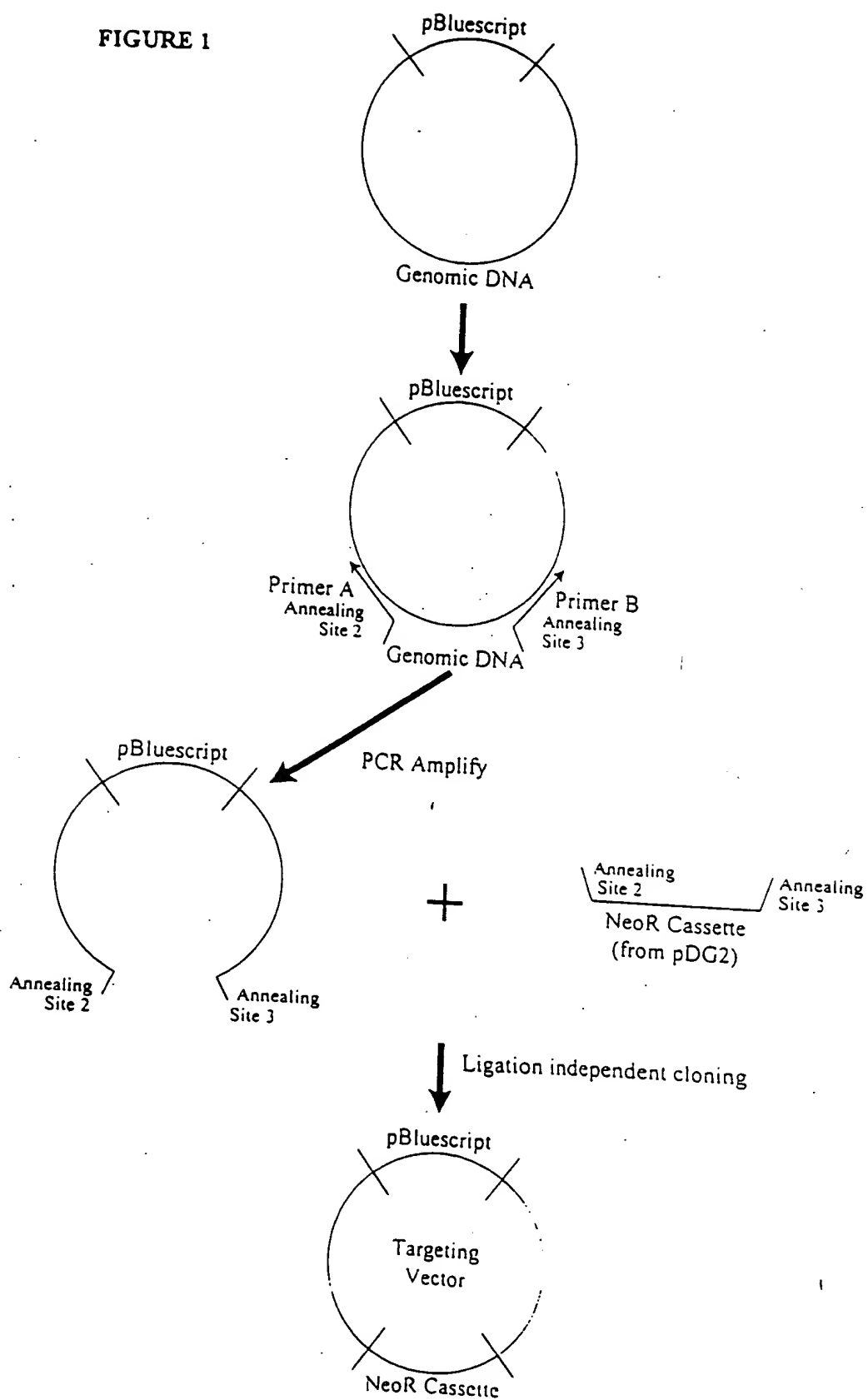


FIGURE 1



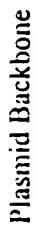


FIGURE 2A

[illegible]

TTTAACTACGTCAGGTGGCCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTGTGTTATTTTCTAAATACATTCAAAATA
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CGTGTCGCGCTTATTCCCTTTTTCGCGGCATTTTGCCTTCTGTTTTGCTCACCAGAAACCGGTGGTGAAGAGTAAAAGA
CTGTGAAGATCAGTTGGGTGACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTGAAGATCCTTGAGAGTTTTCGCC
CCGAAGAACGTTCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTGTGACGCCGGGCA
GAGCAACTCGGTTCGCGCATACATACTTCTAAGATGACTGGTGTGAGTACTCACCAGTCACAGAAAGCATCTTACGGA
TGGCATGACAGTAAGAGAAATTATGCAGTGTCTGCCATAACCTAGGTGAGTACAACCTCGGCCCACTTCTGACACCGA
TCGGAGGACCGAAGGAGCTAACCGCTTTTTCGCAACAATGCGGGATCATGTAACCTCGCTTGATCGTTGGGAACCGGAG
CTGAATGAAGCCATACCAACGACGAGCGGTGACACACGATGCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAAC
TGGCGAACTACTTACTCTAGCTTCCCGGCAACATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGC
TGTCGCGCTTTCGCGGTGGCTGGTTTTATGCTGATAAACTCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCA
CTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGCGGGGAGTCAGGCACTATGGATGAACGAAATAG
ACAGATCGCTGAGATAGGTGCTTCACTGATTAAAGCATTGGTAACCTGTGAGCAAGGTTTACTCATATATACTTTAGATT
ATTTACCCCGGTGATAATCAGAAAGCCCCAAAAACAGGAAGATTGTATAAGCAAAATTTTAAATTGTAAACGTTTAAAT
TTTTGTTTAAAAATTTCGGTTTAAATTTTTGTTTAAATCAGCTCATTTTTTAAACCAATAGGCGGAAATCGGCAAAATCCCTTAT
AAATCAAAAGAAATAGCCCGAGATAGGTTGTAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTTGGACTC
CAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCATGTCGCCCACTACGTTAGACCTACCCAAATCAAGTTTGTGGGGT
CGAGGTGCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCGAACCTTGGCGGA
GAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCAACACA
CCCCCGCGCTTAATGCGCCGCTACAGGGCGCGTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAA
TCTGCTTAACCTGAGTTTTCTGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT
TCGCGCGTAATCTAGTGTCTTTCGCAACAAAAAACCCCGTACAGCGCGGTGGTTTTGTTTCCGGATCAAGAGCTACCAAC
TCTTTTTCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAACTGTTCTTCTAGTGACCGTAGTTAGGCCACC
ACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGCTAATCCTGTTACCAAGTGGCTGCTGCGAGTGGCGCAAG
TCGTGCTTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGCGGTGAACGGGGGGTTCGTGCAC
ACAGCCCAAGCTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCCACGCTTCCCG
AAGGGAAGAAAGCGCAGGTAATCCGTTAAGCGGCGAGGTCGGAACAGGAGCGACCGAGGGAGCTTCCAGGGGAAAC
GCCTGGTATCTTTATAGTCTGTGCGGGTTTCCGCACTCTGACTGAGCGTGAATTTGTGATGCTCTGACGGGGGGG
GAGCTATGGA AAAACCGCAGCAACCGCGGCTTTTTACGGTTTCTGGCTTTTGTGGCTTTTGTCTCAGTGAAGTGTG
AGTTAGCTCACTCATTAGGCCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATA
ACAAATTCACACAGGAACAGCTATGACCACTGATTACGCCAAGCTACGTAATACGACTCACTAGGCGGCGCGTTTAAAC
AATGTGCTCTCTTTGGCTGTCTTCGCGGGCCAAGCCAGACAAGAACCAAGTTGACGTCAAGCTTCCCGGACGCGGTCT
AGCGGCGCGCCGAATTTCTGCAAGGATTCGAGGGCCCCGTCAGGTCAATCTACCGGCTAGGGGAGGCGCTTTTCCCAAGG
CAGTCTGGAGCATGCGCTTTAGCAGCCCCGCTGGCACTTGGCGCTACACAAGTGGCTCTTGGCTCGCCACACATTCACA
TCCACCGGTAGCGCCCAACCGGCTCGGTTCTTTGTTGGCCCCCTTCGCGCCACCTTCTACTCTCCCTAGTCAGGAAGTTT
CCCCCGCGCCCGCAGCTCGCGTCTGTGACGAGCGTGACAAATGGAAGTAGCACGTCTCACTAGTCTCGTGAGATGGACAG
CACCGCTGAGCAATGGAAGCGGGTAGGCTTTTGGGCGAGCGGCCAATGACGAGCTTTGCTCCTTCGCTTCTGGGCTCAGA
GGCTGGGAAGGTTGGTTCGCGGGGCGGCTCAGGGCGGGCTCAGGGCGGGGCGGCGGAAGGTTCTCCGAGGCGCC
GGCATTCTCGCACGCTTCAAAGCGCACGTCTGCCGCGTGTCTCTCTTCTCACTCTCGGGCTTTGCACCTGCAGC
CAATATGGGATCGGCCATTGAACAAGATGGATTGCACGCAGGTTCTCGGCGCGCTTGGGTGGAGAGGCTATTCTGGCTATG
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TTGCGCAGCTGTGCTCGAGCTGTGCTAGCAAGCGGAAGGAGTCTGGTATTTGGGCGAAGTGCAGGGGCGAGGATCTCC
TGTCTCTCACCTTGTCTCTGCGAGAAAGTATCACTATGGCTATGGCTGCAATGGGCGGCTGCATACGCTTGTATCCGGT
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TGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCCGCGAGCTCAAGGCGCGCATGCCCGACGGCGATG
ATCTCGTCTGACCCATGGCGGATGCTGCTTGCAGAAATCATGTTGGAAAAATGGCGGCTTTCTGGATTATCGACTGT
GGCGGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATGCTGAAGAGCTTTGGCGGGAATG
GGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCGATTCGACGCGCATCGCTTCTACTCGCTTCTGACGAGT
TCTTCTGAGGGGATCGATCCGTCTGTAAAGTCTGCAGAAATTGATGATCTATTAAACAATAAGATGTCCACTAAAAATGG
AAGTTTTCTGTGCTACTTTGTTAAGAAAGGGTGAGAACAGAGTACCTACATTTTGAATGGAAGGATTGGAGCTACGGGG
GTGGGGTGGGTGGGATTTAGATAAATGCCGTGCTTTTACTGAAGGCTCTTACTATTGCTTTATGATAATGTTTCATAG
TTGGATATCAATAATTTAAACAAGCAAAACCAATTAAGGGCGAGCTCATTTCTCCCACTCATGATCTATAGATCTATAGA
TCTCTCGTGGGATCATTTGTTTTCTCTGATTTCCACTTTGTGGTTCTAAGTACTGTGGTTTTCCAAATGTGTGAGTTCTCA
TAGCTTGAAGAACGAGATCAGCAGCCTCTGTTCCACATACACTTCTTCTCAGTATGTTTTGCCAAGTTCTAATTTCCAT
CAGAAGCTGACTCTAGATCTGGATCCGGCCAGCTAGGCCGTGCAGCTCGAGTGTATCAGGTACCAAGGTCCTCGCTCTGTG
TCGGTTGAGCTCGACGACAGGACAGCGAAATTAATTAAGGCCGGGCGGTACCTCTAGTCAAGGCTTAAAGTGTGAGTCTG
TATTACGGAATGGCGCTCGTTTTACAACGTGCTGACTGGGAAAAACCTTGGCGTTACCCCACTTAATCGCCTTGCAGCACA
TCCCCCTTTCGCGACGTCGGGTAATAGCGAAGAGGCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAAATGGCG
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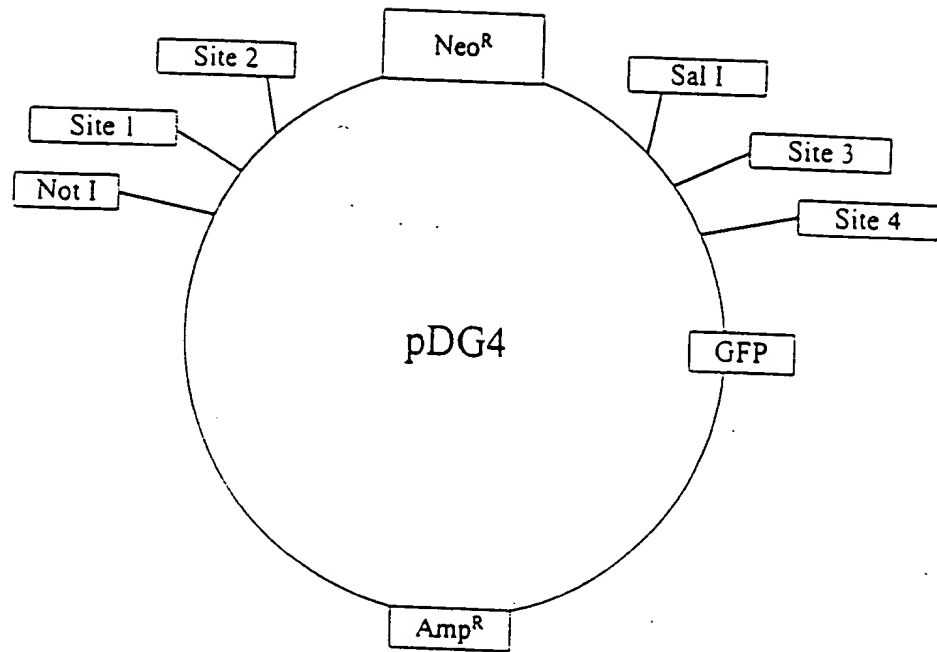


FIGURE 3A

[illegible][illegible]

TGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGGCGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
 ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA
 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCGACGGCGATGATCTCGTCGTGAC
 CCATGGCGATGCCTGCTTGCGAATATCATGGTGGAAAATGGCCGCTTTCTGGATTCTCGACTGTGGCCGGCTGGGTG
 TGGCGGACCGCTATCAGGACATAGCGTGGCTACCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC
 CTCGTGCTTTACGGTATCGCGCTCCCGATTCCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGGGGA
 TCGATCCGTCTCTGAAGTCTGCAGAAATTGATGATCTATTAAACAATAAAGATGTCCACTAAAATGGAAGTTTTCTGT
 CATACTTTGTTAAGAAGGGTGAGAACAGAGTACCTACATTTTGAATGGAAGGATTGGAGCTACGGGGTGGGGTGGGGT
 GGGATTAGATAAATGCCTGCTCTTTACTGAAGGCTCTTTACTATTGCTTTATGATAATGTTTCATAGTTGGATATCATAA
 TTTAAACAAGCAAAACCAAATTAAGGGCCAGCTCATTCTCCCACTCATGATCTATAGATCTATAGATCTCTCGTGGGAT
 CATTGTTTTCTCTTGATTCCCACTTTGTGGTTCTAAGTACTGTGGTTTCAAATGTGTGAGTTTCATAGCTGAAGAAC
 GAGATCAGCAGCCTCTGTTCCACATACACTTCATTCTCAGTATTGTTTTGCCAAGTTCTAATTCATCAGAAGCTGACTC
 TAGATCTGGATCCGGCCAGCTAGGCGGTCGACCTCGAGTGATCAGGTACCAAGGTCCTCGCTCTGTGTCCGTTGAGCTCG
 ACGACACAGGACACGCAAATTAATTAAGGCCGGCCGCTACCTCTAGTCAAGGCTTAAGTGAGTCGTATTACGGACTGG
 CCGTCGTTTTACAACGTCTGACTGGGAAAACCTGGCGTTACCCAACCTTAATCGCCTTGCGAGCATCCCCCTTTCCGC
 AGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTCGC
 TTGGTAATAAAGCCCGCTTCGGCGGGCTTTTTTTT

FIGURE 3B (Continued)

003607 3336360

Annealing site	Sequence	Sequence after digestion
1	5' tgtgctcctcttttggttgcttccaa... 3' 3' acacgaggagaaaccgaacgaagggtt... 5'	5' tgtgctcctcttttggttgcttccaa... 3' 3' tt... 5'
2	5' ctggttctctgtctggttggtcccaa... 3' 3' gaccaagaacagaccgaaccgggtt... 5'	5' ctggttctctgtctggttggtcccaa... 3' 3' tt... 5'
3	5' ggtcctcgctctgtgtccggttgaa... 3' 3' ccaggagcgagacacagggcaactt... 5'	5' ggtcctcgctctgtgtccggttgaa... 3' 3' tt... 5'
4	5' ttgcggtgctcctgtgtcgtcgaa... 3' 3' aaacgcacaggacacagcagctt... 5'	5' ttgcggtgctcctgtgtcgtcgaa... 3' 3' tt... 5'

FIGURE 4

Annealing site	Sequence	Sequence after digestion
1	5' AATgtgctcctcttcttggccttgcttccgc 3' 3' Ttacacgaggagaaacccaacgaagg 5'	5' AA 3' 3' Ttacacgaggagaaacccaacgaagg 5'
2	5' AActggttcttctgtctgtgcccgc 3' 3' Ttgaccaagaacagaccgaaccggg 5'	5' AA 3' 3' Ttgaccaagaacagaccgaaccggg 5'
3	5' AAggtcctcgcctctgtgtccgcttGAGCT 3' 3' Ttccaggagcgagacacaggcaac 5'	5' AA 3' 3' Ttccaggagcgagacacaggcaac 5'
4	5' AAttgctgtcctgtgtgtcgtcGAGCT 3' 3' Ttaaacgcacaggacacagcagc 5'	5' AA 3' 3' Ttaaacgcacaggacacagcagc 5'

FIGURE 5

FIGURE 6

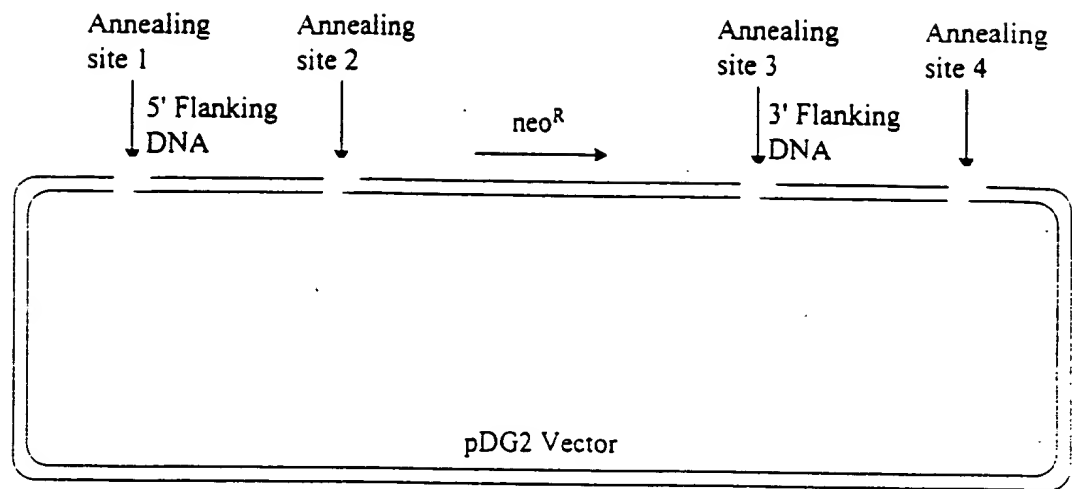


FIGURE 7

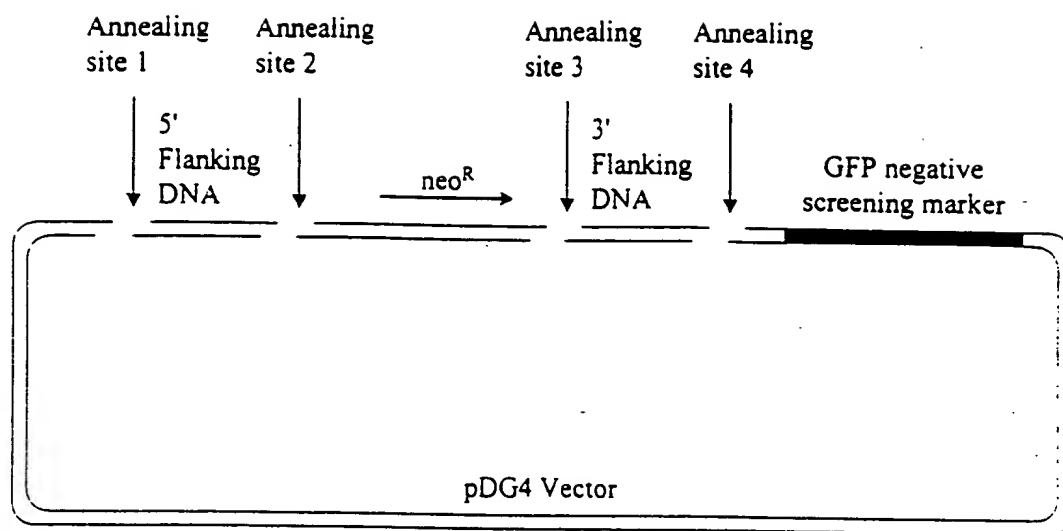


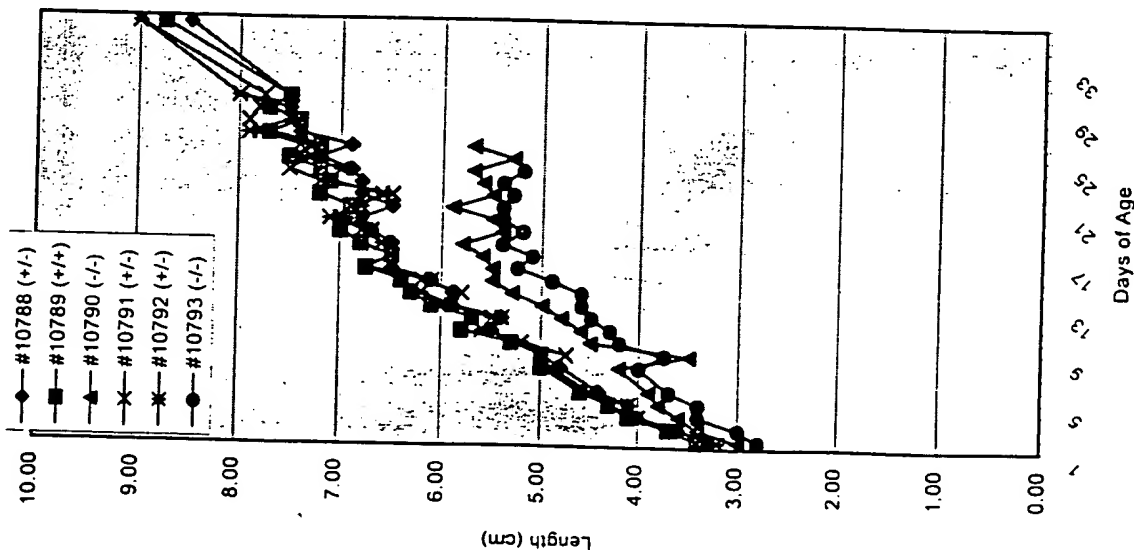
FIGURE 8

Oligo #	Sequence (5' to 3')
174	ATGACCGCTCAGGAAACCTGTTGCA
180	ATAGGCATAGTAGGCCAGCTTGAGG
454	tgtgctcctctttggcttgcttccAATTAACCCTCACTAAAGGGAACGAAT
463	ctgggttcttgtctggcttggcccaaTGCAACAGGTTTCCTGAGCGGTCAT
464	ggtcctcgctctgtgtccgttgaaCCTCAAGCTGGCCTACTATGCCTAT
42	tttgcggtgctctgtgtcgctcgaaCGACTAATACGACTCACTATAGGGCG
151	GCCAATGGACTCTTAGTTTTGGAAC
155	GTTCTGGCAAACAAATTCGGCGCAC
454	tgtgctcctctttggcttgcttccAATTAACCCTCACTAAAGGGAACGAAT
465	ctgggttcttgtctggcttggcccaaGTTCCAAACTAAGAGTCCATTGGC
466	ggtcctcgctctgtgtccgttgaaGTGCGCCGAATTTGTTTGCCAGAAC
1	GAACCTTGGTGTGCCAAGTTACTTC
2	GAACCTTGGCTGAACCCCTTGTTCT
41	tgtgctcctctttggcttgcttccAATTAACCCTCACTAAAGGGAACGAAT
38	ctgggttcttgtctggcttggcccaaGAAGTAACTTGGCACACCAAGGTTTC
40	ggtcctcgctctgtgtccgttgaaAGAACAAGGGGTTTCAGCCAAAGTTC
37	tttgcggtgctctgtgtcgctcgAATTAACCCTCACTAAAGGGAACGAAT
540	ATGCCGGATCTCCTACTACTGGGCC
546	TGTCATAGTAGACAGCGATGGAACG
445	GACAAGAACCAGTTGACGTCAAGCTTCCCGGGACGCGTGCTAGCGGCGCGCCG
667	ctgggttcttgtctggcttggcccaaGGCCAGTAGTAGGAGATCCGGCAT
668	ggtcctcgctctgtgtccgttgaaCGTTCCATCGCTGTCTACTATGACA
907	ctgggttcttgtctggcttggcccaaAAAGCCGACAGCCACGCTCACAAGC
908	ggtcctcgctctgtgtccgttgaaGCCCAATGCCACAGAGAGAGAATGT
1157	ctgggttcttgtctggcttggcccaaGTTGGATCCTCTCCAAGGCCCATCT
1158	ggtcctcgctctgtgtccgttgaaCTCCAGTGCCGAGTGTGTGGGGACAG

009307 9896960

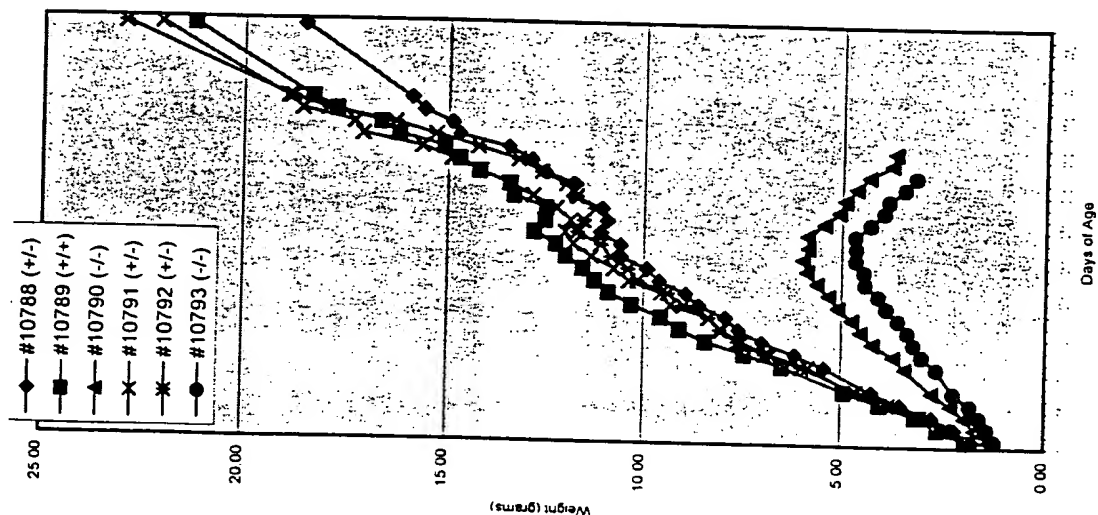
T243 ES242 Mating #1799

Progeny Lengths



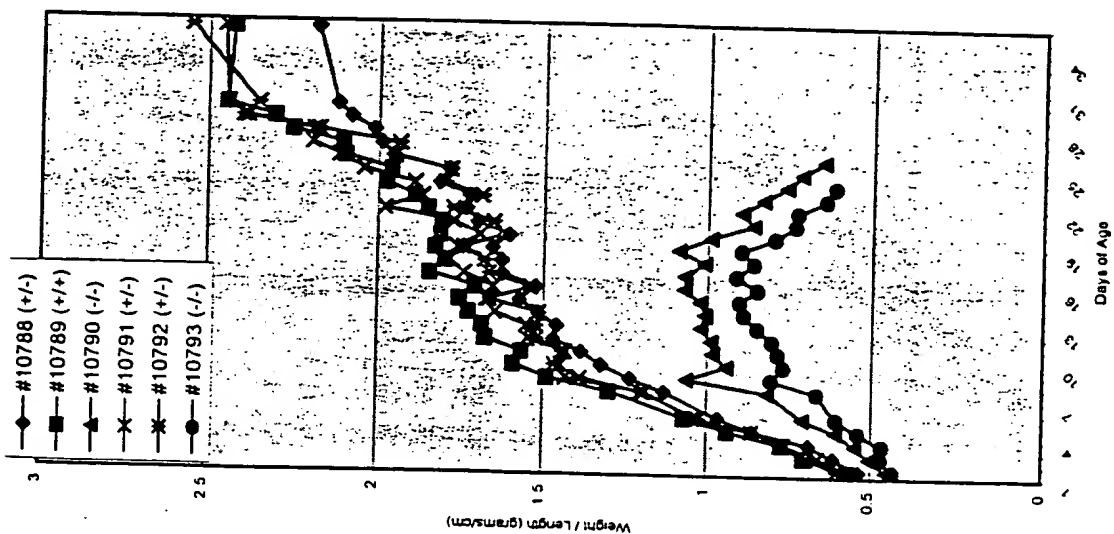
T243 ES242 Mating #1799

Progeny Weights

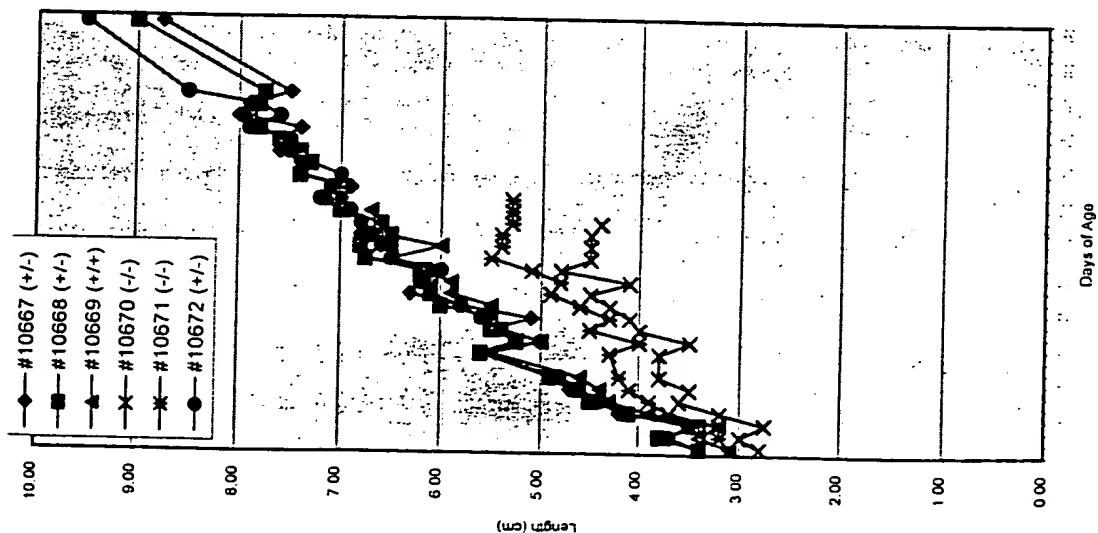


T243 ES242 Mating #1799 Progeny

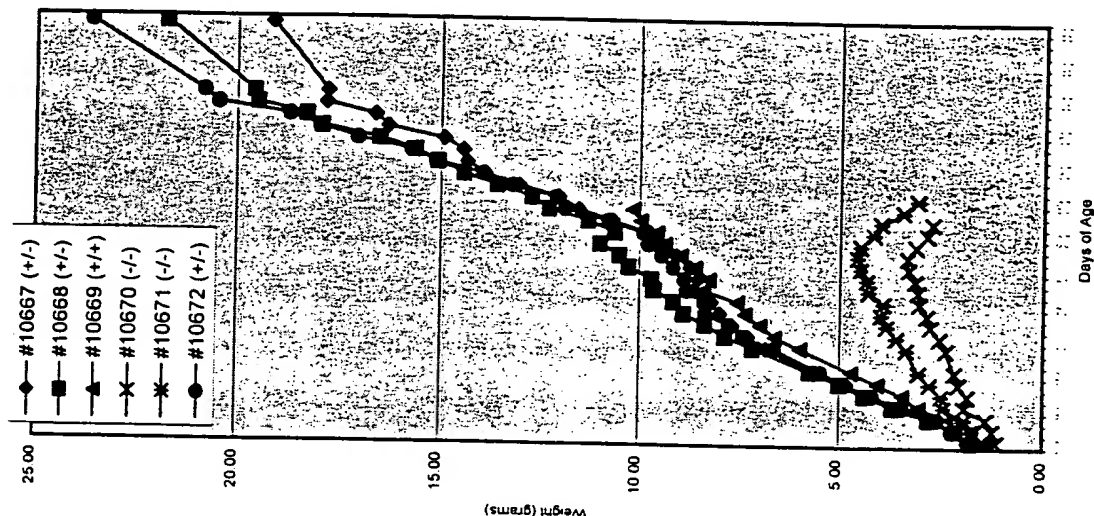
Weight / Length



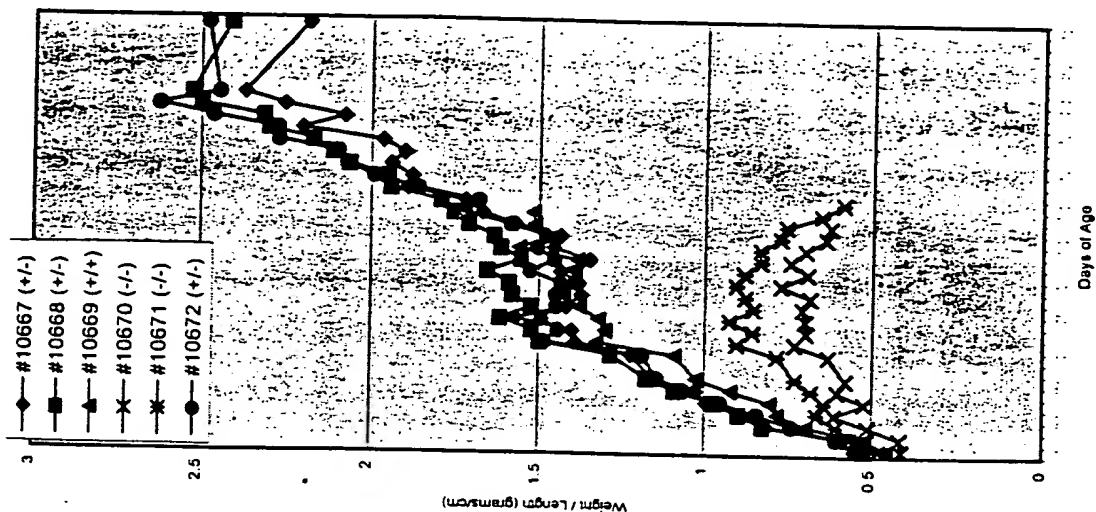
T243 ES242 Mating #1808
Progeny Lengths



T243 ES242 Mating #1808
Progeny Weights



T243 ES242 Mating #1808
Progeny Weight / Length



[illegible]

GGCACGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCATGTCTG
AGCTCGCGCCCCGCTGCCTCTTATTTCCCTTTGCTGCTGCTGCTTCCGCTGCTGCTCCTTCCCTGCCCGAA
GCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTGCGATTGCCAGCAAATGCGAAGTGTGC
AAGTATGTTGCTGTGGAGCTGAAGTCCGGCTTTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCG
GCTATGGCATCCTGGACGGGAAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGT
CACTGAGACCATTGTGAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTT
GCCAAGGGTATGTGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAGGGGTCAAGGTGGTGATGG
ATATCCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTGACGTGCT
GGTGGAAGAGTTTGAAGAGGTTGATTGAGGACTGGTACAGGAACCCACGAGGAGGAAGACCTGACTGAATTC
CTCTGTGCCAACACGTGCTGAAGGGAAGGACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAG
GGGACATAGCCTCCCTGGGAGGGAAGAAATCCAAGAAGAAGCGCAGCGGAGTCAAGGGCTCCTCCAGTGG
CAGCAGCAAGCAGGGAAGGAAGTCTGGGGGCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGGTGTG
CAGAAGGACATCGCCCCCTCCACACAGCCCCCTGATGAGCTGTGAGCCAGCTTAGTGTCTTGAATCAA
GACCCCTGACTTCAGAGCTTGGGACACGCACAGCGCAGCGCAGCGCAGCTCCAGCAAGGACAGCTGCTGT
CCAGCATCAGGTCTCCTCCCTTGGCTGTGCCCTTTCTTCCCTTGAACAACAGCAAGAGGTGGAAGGAT
CTGGGGTGTCTGGGAGACGGCACCCCAAAGGGAAGAGGAGGAGGAGCAGAAGGCAGCTCTCTTTCTACACA
GTCCCCCTCAGAGCTCCGGGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCT
GAAGAGCATGAGGCACATAAGATGCTCACCAGCGCCCCCTTACGCCAGGAAGGACTCCGTGCAGCCTCAG
CAGCCAGGCTGCCTCTTCTTCCACCAAGCATTCTCTTCTGCTGGTCTTGTGGATGGTAAATTTCGAG
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CAGAGAGGGCACCTGACCTAACCCCCCTGGAAAGCCAATCTGCAGTTCCTCGTGTCCACCCACTCCTCCTG
AGGACGCCCTCATGCTCTGCCCAGCCCTTCTCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTTTCGGT
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CAGGGGTGGAAGGCCATCACCATTCAATGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGGAGCGCC
CGGGGTGTTGTTGGGGTAATCACTCACTGGCTCTCAGCCTTCTAACACTGCAGCCCCCTTAATACAGTTCC
TTCTGTTGTGGTGACTCCACGCCCCCACACACACACCATAAAATTATTTTCGATGCTGTTTCATAACTGT
AAAAAAAAAAAAAAAAAAAA SEQ ID NO:47

CGAGCCATGGATTCAATGCGCTGAGCCCGCGTCCCGCTGTCTTCTGCTTCTTCCCTTGCTGCTGCTGCTGCTG
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GCCCAGCAAAATGCGAAGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAG
ACCAAGGAGGTGATTGGCACGGGCTATGGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGT
CGGACTTGCGGTTAATCGAAGTCACTGAGACCATTTCGAAGAGGCTCCTGGATTATAGCCTGCACAAGGA
GAGGACCGGCAGCAATCGATTTGCCAAGGGCATGTGAGAGACCTTTGAGACATTACACAACCTGGTACAC
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GAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAGAAGTCCAAGAAGAAGAGCAGCA
GGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAAACAAAGGAAGGAGCTGGGTGGCCTTGAGGGAGA
CCCCAGCCCCGAGGAGGATGAGGGCATCCAGAAGGCATCCCCCTCTCACACACAGCCCCCTGTATGAGCTC
TGAGCCCACCCAGCATCCTCTGTCTTGAGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTG
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MDSMP^{EPAS}RC^{LLLL}PL^{LLLLLLLLLL}PA^{EL}GP^{SQAGAE}END^{WVRL}PS^{KCE}
V^{KY}V^{AVEL}KS^AFE^{ET}G^{KT}KE^{VI}GT^{GY}G^{ILD}Q^{KAS}G^{VKY}T^{KSD}LR^LIE^{VT}
ET^{ICK}RL^{LD}YS^LHK^{ERT}GS^NRF^{AK}GM^{SET}F^{ET}L^{HN}L^{VH}K^GV^{KV}MD^IPI^{YE}
L^{WN}ET^{SA}E^{VAD}L^{KK}Q^{CD}VL^{VEE}F^EEE^VIE^DW^{YRN}H^QE^{ED}LT^EFL^{CAN}H^{VL}K
G^{KD}T^{SCL}A^{EQ}W^{SG}K^GGD^TA^{AL}G^GK^KS^{KK}SS^{RA}K^AAG^{GR}SS^{SS}S^KQ^RKE^LG
GLE^{GD}PS^{PEE}DE^{GI}Q^{KAS}PLTHSP^{DEL} SEQ ID NO:58

[illegible]

FIGURE 13

AGCTCAGACATGGACTCCATGGCCC SEQ ID NO:45

TGCGATTGCCCAGCAAATGCGAAGT SEQ ID NO:46

Outward oligo 488 ctggttcttgtcggcttggcccaaAGCTCAGACATGGACTCCATGGCCC
SEQ ID NO:48

Outward oligo 489 ggtcctcgctctgtgtccgttgaaTGCGATTGCCCAGCAAATGCGAAGT
SEQ ID NO:49

primer 426 GGGCCATGGAGTCCATGTCTGAGCT SEQ ID NO:55

primer 432 ACTTCGCATTTGCTGGGCAATCGCA SEQ ID NO:56

003607-303600

FIGURE 14

5' of the deletion:

ACAGAAAACAAGAAACAAAAACCATGAAAGATAGTCTGTTATCCAGGGCTAGAATGCCCAAGGCTGGTT
CATCCAAGGTATGATGAAGGTTCAACCCGCTAGGAACTGATGCTCCAGCTACTGAGCCTCCTTTAGCTGGC
AGTGATATCGCTATAGGGCGCCAAAGCCACCATCCGCTCTCTGATTGGGTGAGATGGGAAAAAAAAAAGA
TAGTTCCTCTCATTGGCTATAAAGCAGACGCCGAGCGAACCATTGGTTGNGTCGCCCCGCGGCCTTGGT
CGGTTTCGCAAGCCGCTAGAGGCTACCGGGCGAGGGCGGGCCGAGCTCGCCGTTGCCGTGGTTACCCA
GAGACACGTGCGCAGTCCCGGAAGCGGCCGGGGGAAGCTGCTCCGCGCGCTGCCGAGGAAGCGCCGC
CGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCATGTCTGAGCT_ 3' SEQ ID NO:50

3' of the deletion:

5'

TGCGATTGCCCAGCAAATGCGAAGGTGAGGGGGCGGGGCCGCGGGGCGTAGCCAAGCCCCGAGGGGCGGGA
GGGGGCGGGGCTGTGGGAAGGGTCTGGGCCTGGCAGGACCTGGGCTGGGGTCTCCTTGGCCCTGCTGTG
TGCTTTGCGGCAATGCTGGGTGCTGTGACTCTCGGATAACCTGGAGATCCCTGCTTTTGGGCGAATCCGG
GGGTAGTTGCTCATCAAGACTAGAGGTGGGGGTGGAGGGAAGGCTTCATACAGGAAGCCTGCTGCGAAAT
GAAGAGTTGGCCAGGGAAGCATGGCGTGCAGAGGAACCTCACTCCGCAGAAACCACAGAAACAGAGGCAG
ATGAGGACGCCCTGCCGGCC 3' SEQ ID NO:51

CGCGTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCATGTCTGAGCT_ 3' SEQ ID NO:50

5'

Expanded T243

$\{f^{(n)}_i\}_{i=1}^m$ are the functions $f^{(n)}_i$ and $\{g^{(n)}_i\}_{i=1}^m$ are the functions $g^{(n)}_i$ in the space $L^2(\Omega)$. The functions $f^{(n)}_i$ and $g^{(n)}_i$ are defined by the following formulae:

$$f^{(n)}_i(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} f_i(t) e^{itx} dt, \quad g^{(n)}_i(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} g_i(t) e^{itx} dt,$$
 where f_i and g_i are the functions f_i and g_i in the space $L^2(\Omega)$. The functions $f^{(n)}_i$ and $g^{(n)}_i$ are defined by the following formulae:

$$f^{(n)}_i(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} f_i(t) e^{itx} dt, \quad g^{(n)}_i(x) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} g_i(t) e^{itx} dt,$$
 where f_i and g_i are the functions f_i and g_i in the space $L^2(\Omega)$.

Amino Acid Sequence

MESMSSELLRPSKCEVCKYVAVELKS SAFEETG
KTKEVIDTGYGILDGKGSGVKYTKSDLRLIEVTETICTKRLLDYSLHKERTGSNRFAGKMSETFETLHNLV
HKGKVVM DIPYELWNETS AEVADLKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLCANHV LKGKDT SCL
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SEQ ID NO:54